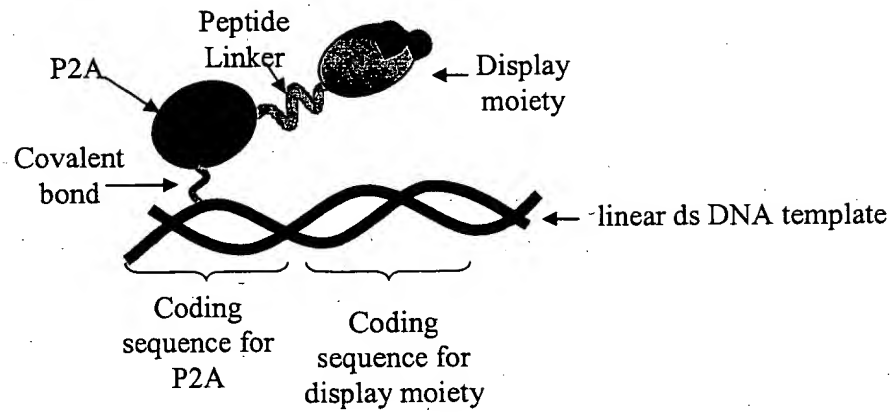

Figure 1. Covalent display
Double stranded DNA containing the coding sequence for P2-A and the coding sequences for a diverse population of polypeptides is transcribed and translated *in vitro* and due to the cis-activity of P2-A, the expressed polypeptides spontaneously and covalently associate with their own encoding DNA molecules through the interaction between P2-A and its recognition sequence which is contained within the P2-A gene. The covalent Protein-DNA complexes are then used in affinity selection protocols against a given target in order to identify individual genes that encode ligands to the target.

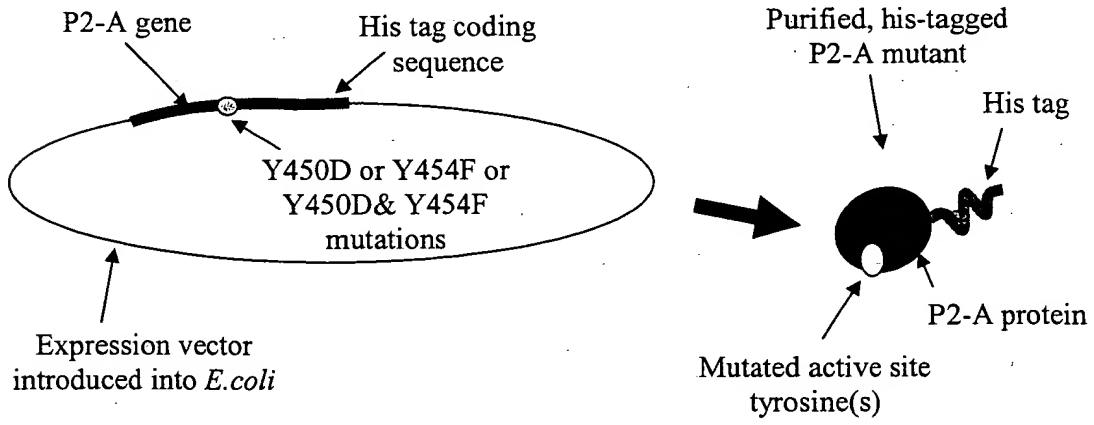

Figure 2. Liu's disclosure
P2-A wild type sequence, or P2-A genes in which either the putative active site tyr450, the putative active site tyr454 or both putative active site tyrosines were mutated, were cloned in frame with a hexa-histidine tag. The expressed polypeptides from these constructs formed inclusion bodies from which purified P2-A variants were isolated and used in biochemical analyses of the catalytic mechanism of P2-A. No attempt to isolate covalent complexes consisting of the P2-A gene and the expressed P2-A protein was made. No diverse population of P2-A-fused binding domains was made. No indication was made that the cis property of P2-A could be exploited for the establishment of a library screening method.

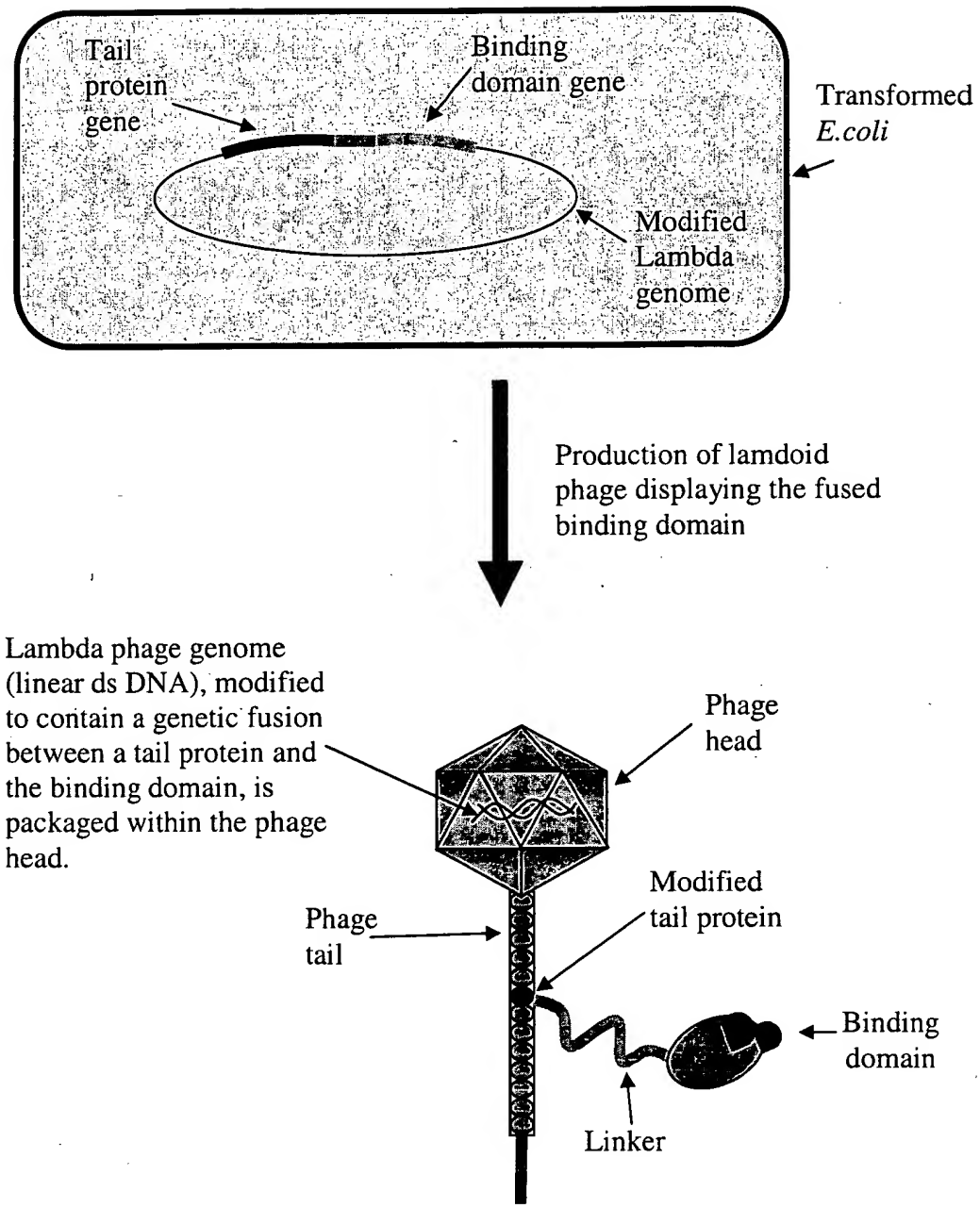

Figure 7. Lambdoid display
The coding sequences for a diverse population of polypeptides are fused in frame with the gene encoding the tail protein of phage lambda. Upon production on new phages, the modified genome is packaged into the phage head while the displayed polypeptide is fused to a tail protein in such a way that it is accessible for interaction with external binding partners. The phages so generated are then used in affinity selection protocols against a given target in order to identify individual genes that encode ligands to the target.